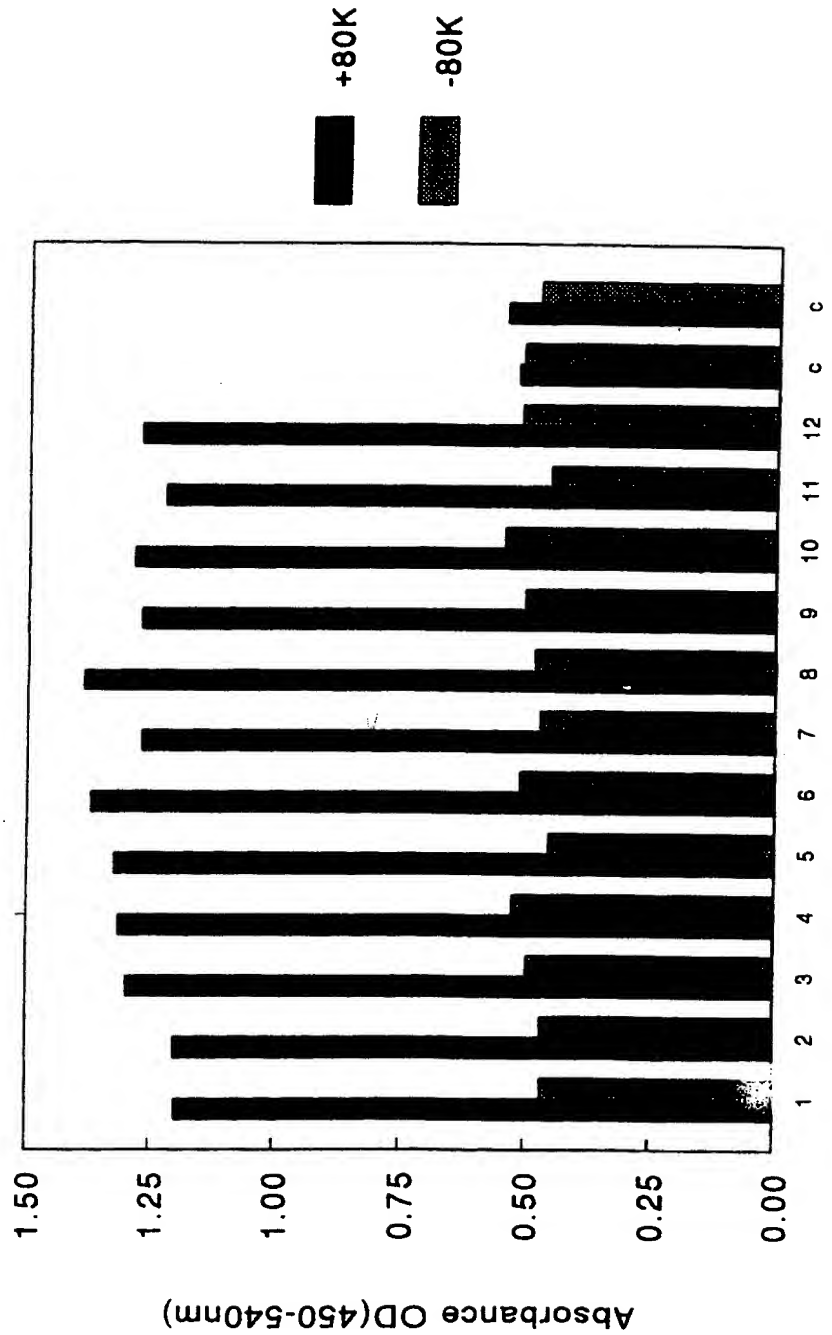

+80K
-80K
Absorbance OD(450-540nm)
1.50
1.25
1.00
0.75
0.50
0.25
0.00
1
2
3
4
5
6
7
8
9
10
11
12
c
c
c
clone

Figure 1

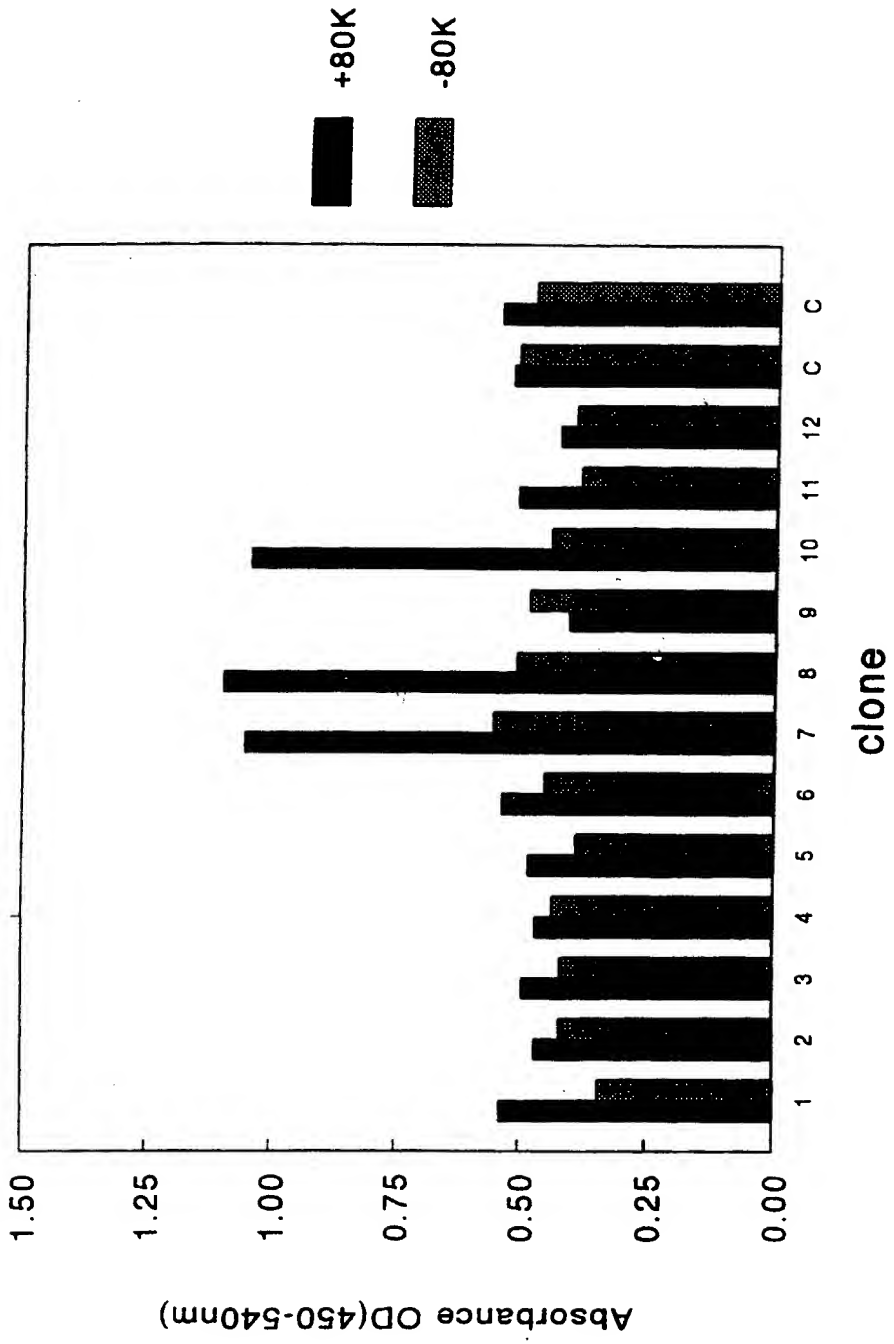

+80K
-80K
1.50
1.25
1.00
0.75
0.50
0.25
0.00
Absorbance OD(450-540nm)
1
2
3
4
5
6
7
8
9
10
11
12
C
C
C
clone

Figure 2

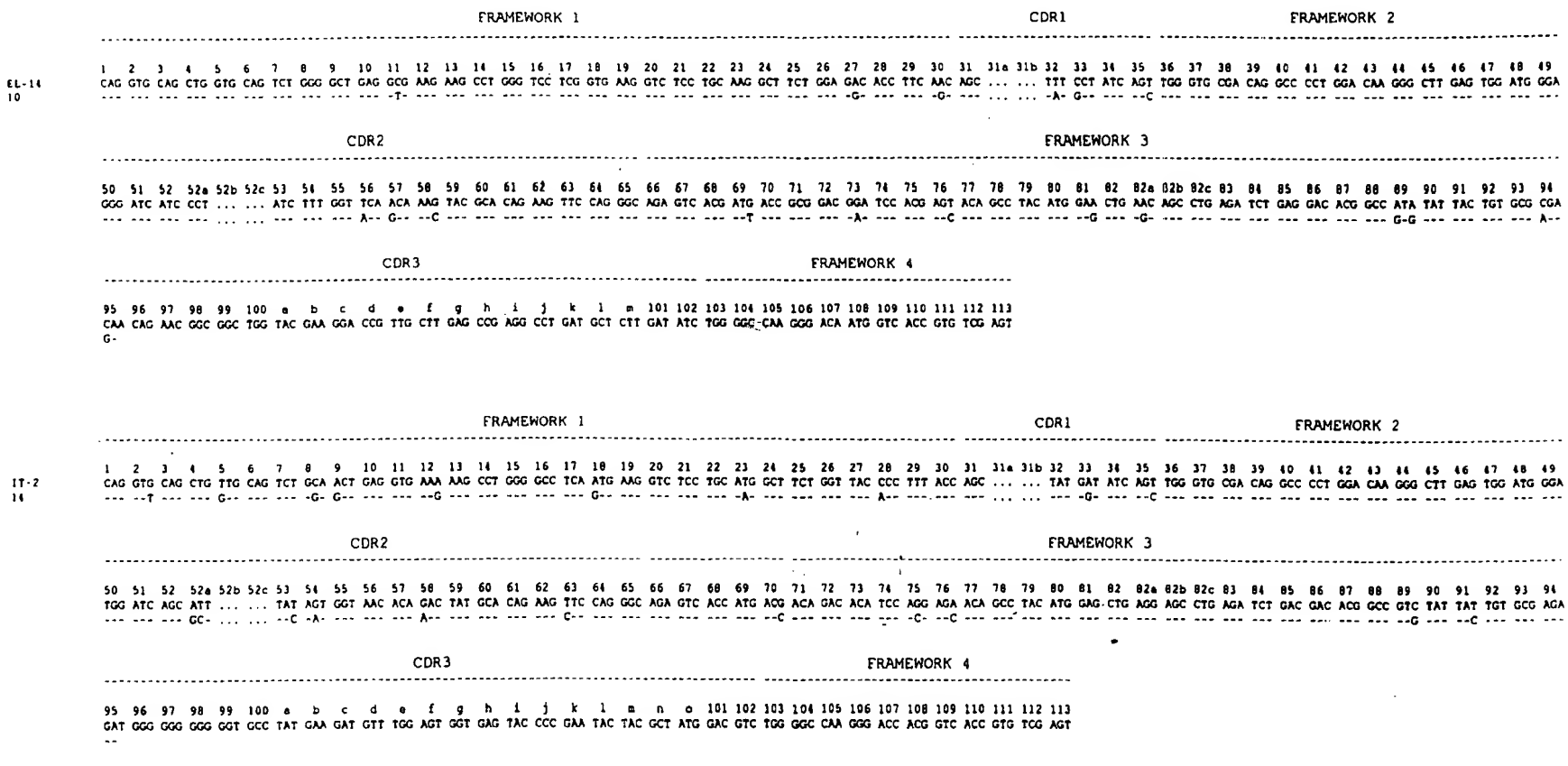

FRAMEWORK 1
CDR1
FRAMEWORK 2
CDR2
FRAMEWORK 3
CDR3
FRAMEWORK 4
EL-14
10
IT-2
14

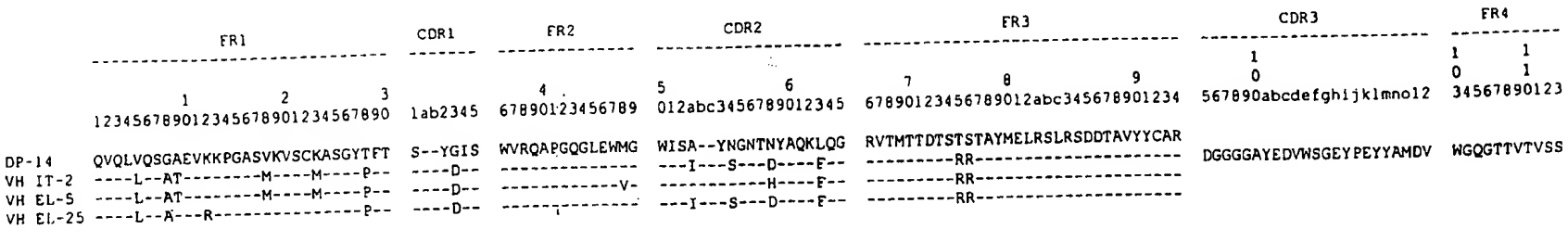
Figure 3

SUBSTITUTE SHEET (RULE 26)

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 2 3 12345678901234567890123456789O	1ab2345	4 67890123456789	5 6 012abc3456789012345	7 8 9 678901234567890123abc345678901234	1 0 567890abcdefghijklm12	1 1 0 1 34567890123
VH EL-14	QVQLVQSGAEAKKPGSSVKVSCKASGDTFN	S--FPIS	WVRQAPGQGLEWMG	GIIP--IFGSTKYAQKFQG	RVTMTADGSTSTAYMELNSLRSEDTAIYYCAR	QQNGGWYEGPLLEPRPDALDI	WGQGTMVTVSS
DP-10	----------V----------G--S	---YA--	----------	---------TAN--------	---I---E---------S--------V-----		

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 2 3 12345678901234567890123456789O	1ab2345	4 67890123456789	5 6 012abc3456789012345	7 8 9 678901234567890123abc345678901234	1 0 567890abcdefghijklmnol2	1 1 0 1 34567890123
VH IT-2	QVQLLQSATEVKKPGASMKVSCMASGYPFT	S--YDIS	WVRQAPGQGLEWMG	WISI--YSGNTDYAQKFQG	RVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR	DGGGGAYEDVWSGEYPEYYAMDV	WGQGTTVTVSS
DP-14	----V--GA--------V----K----T--	----G--	----------	---A---N---N----L--	---------TS----------		

Figure 4A



	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 2 3 12345678901234567890123456789O	1ab2345	4 678901234567 89	5 6 012abc3456789012345	7 8 9 67890123456789012abc345678901234	1 0 567890abcdefghijklmnol2	1 1 0 1 34567890123
DP-14	QVQLVQSGAEVKKPGASVKVSCKASGYTFT	S--YGIS	WVRQAPGQGLEWMG	WISA--YNGNTNYAQKLQG	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	DGGGGAYEDVWSGEYPEYYAMDV	WGQGTTVTVSS
VH IT-2	----L--AT--------M----M----P--	----D--	----------	---I---S---D----E--	---------RR----------		
VH EL-5	----L--AT--------M----M----P--	----D--	----------V-	----------H----E--	---------RR----------		
VH EL-25	----L--A---R----------P--	----D--	----------	---I---S---D----E--	---------RR----------		

Figure 4B

SUBSTITUTE SHEET (RULE 26)

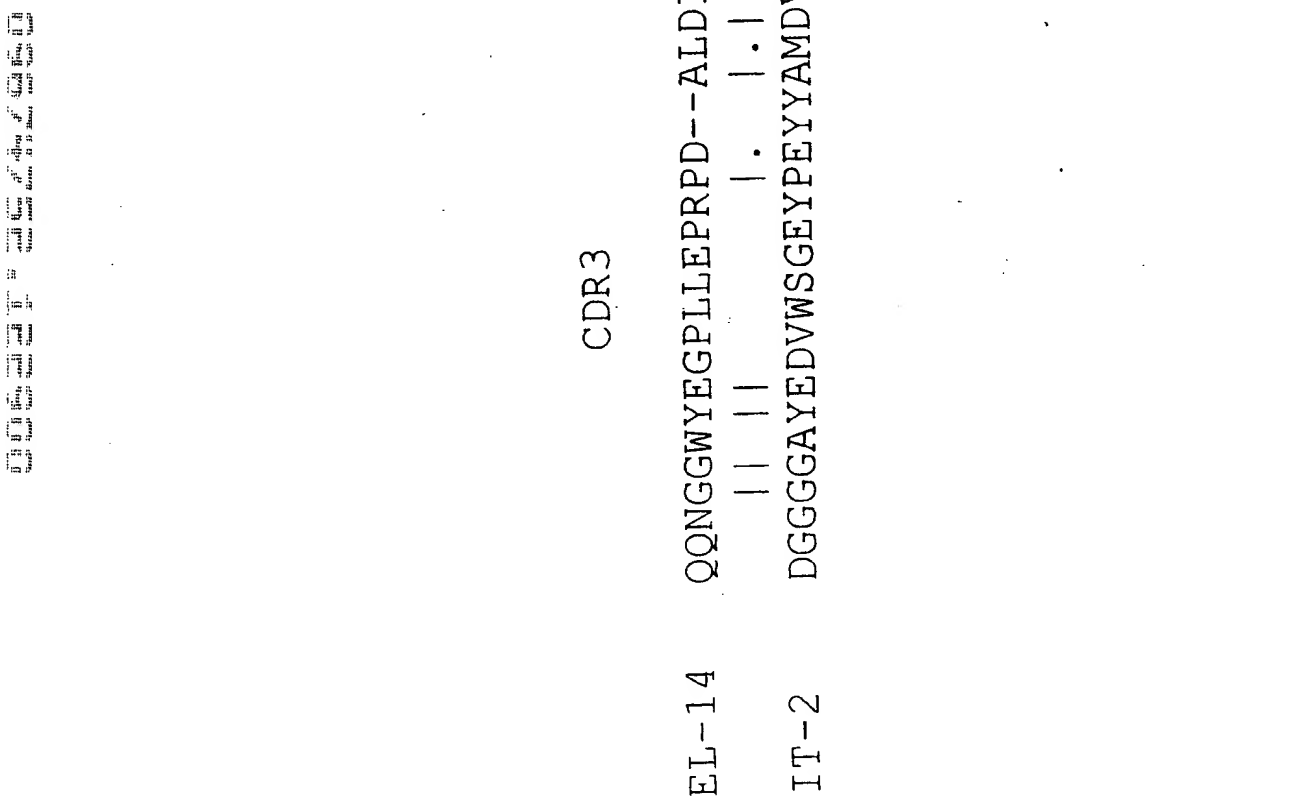

CDR3
EL-14 QQNGGWYEGPLLEPRPD--ALDI
IT-2 DGGGGAYEDVWSGEYPEYYAMDV

Figure 4C

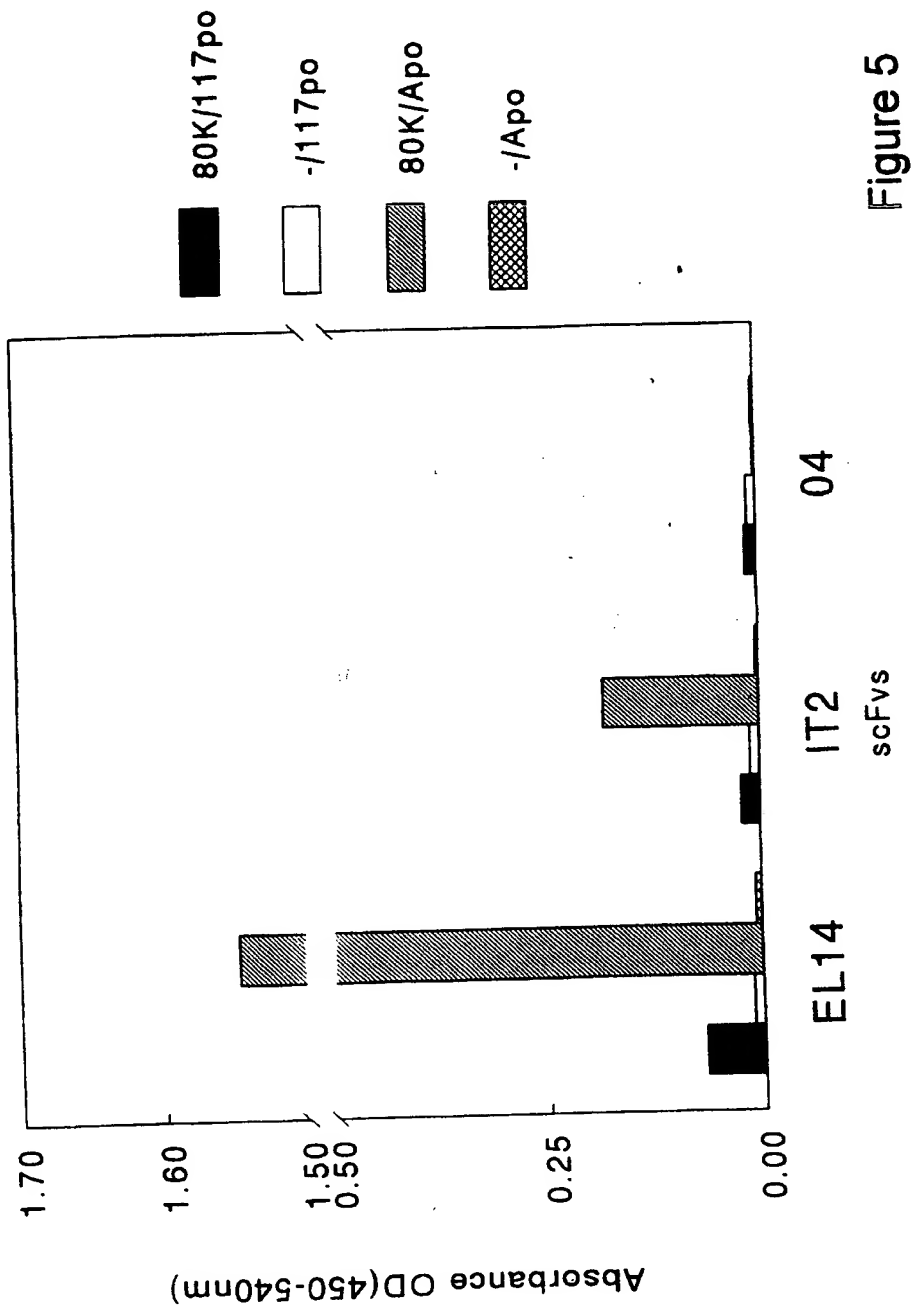

80K/117po
-/117po
80K/Apo
-/Apo
EL14
IT2
04
scFvs
1.70
1.60
1.50
0.50
0.25
0.00
Absorbance OD(450-540nm)

Figure 5

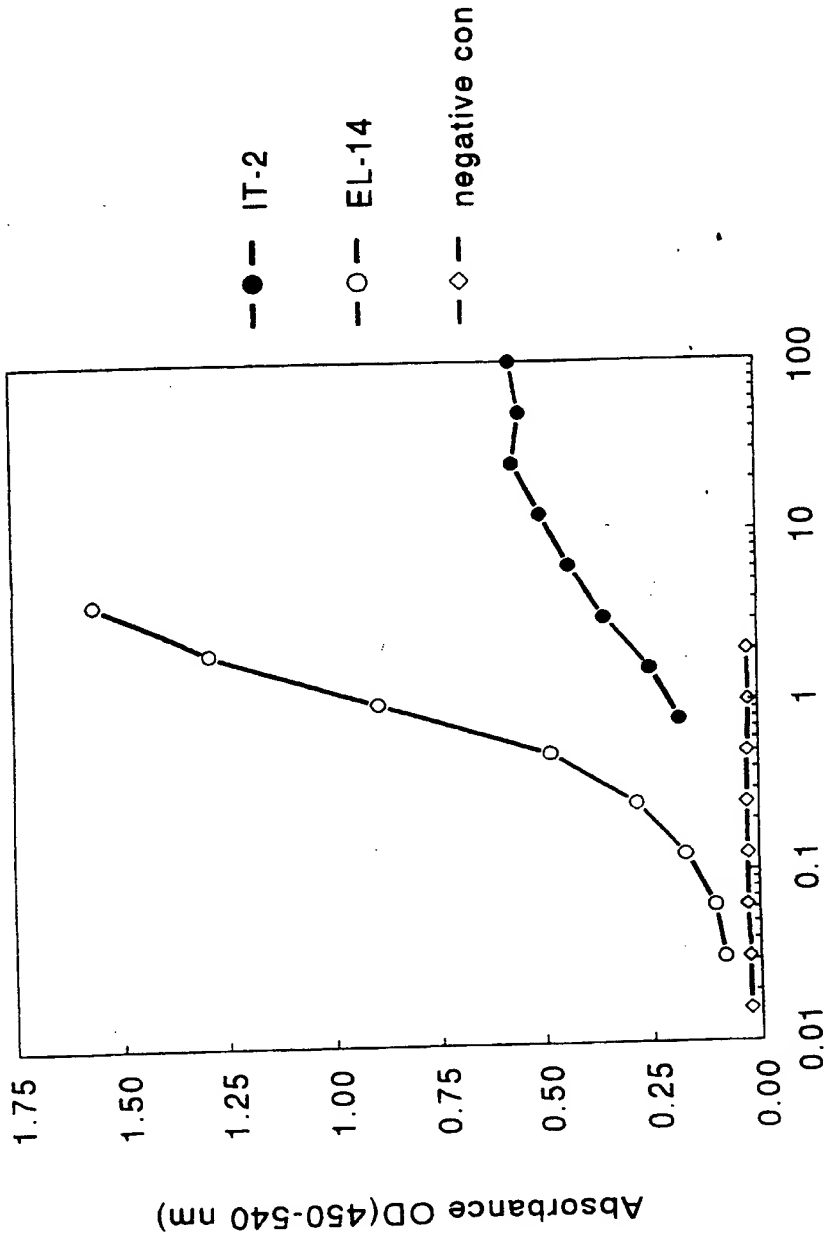

IT-2
EL-14
negative con
Absorbance OD(450-540 nm)
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
0.01
0.1
1
10
100
Concentration (µg/ml)

Figure 6

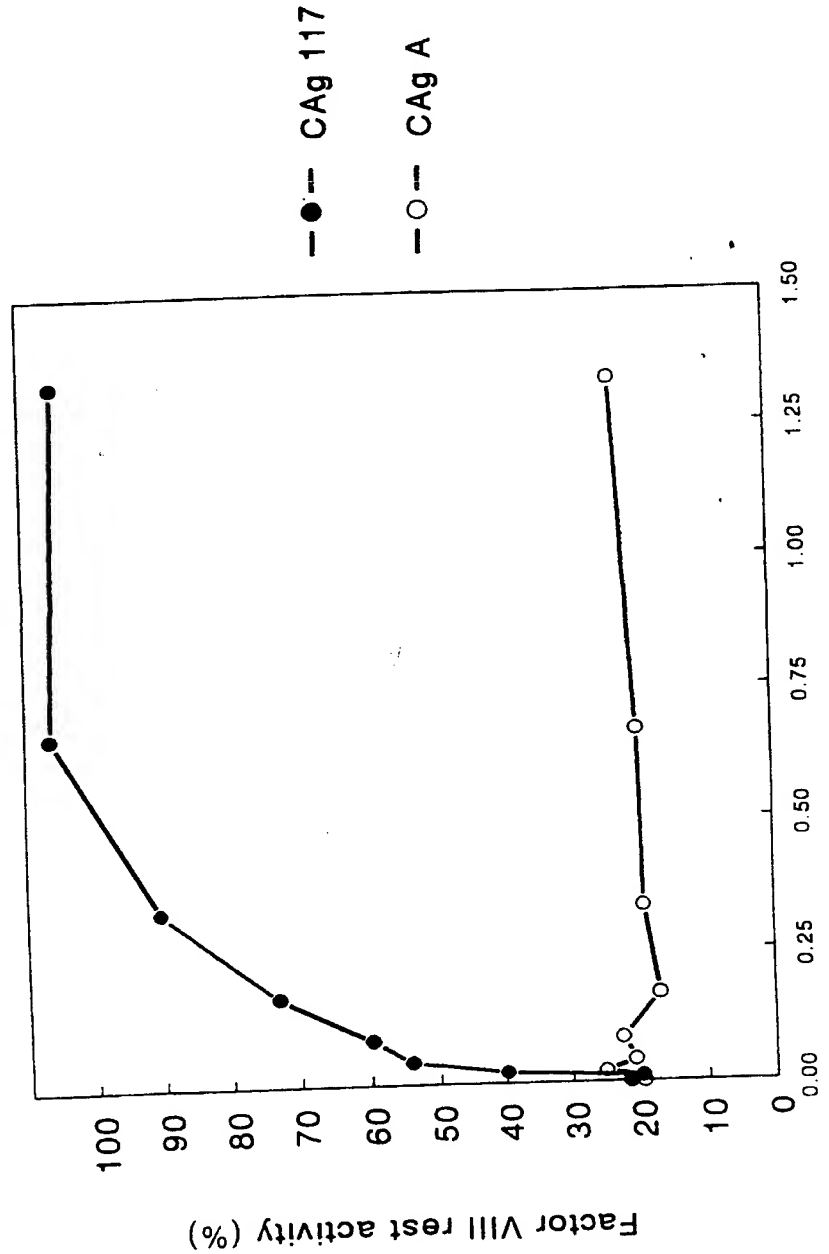


Figure 7A NEUTRALIZATION BY scFv EL-14

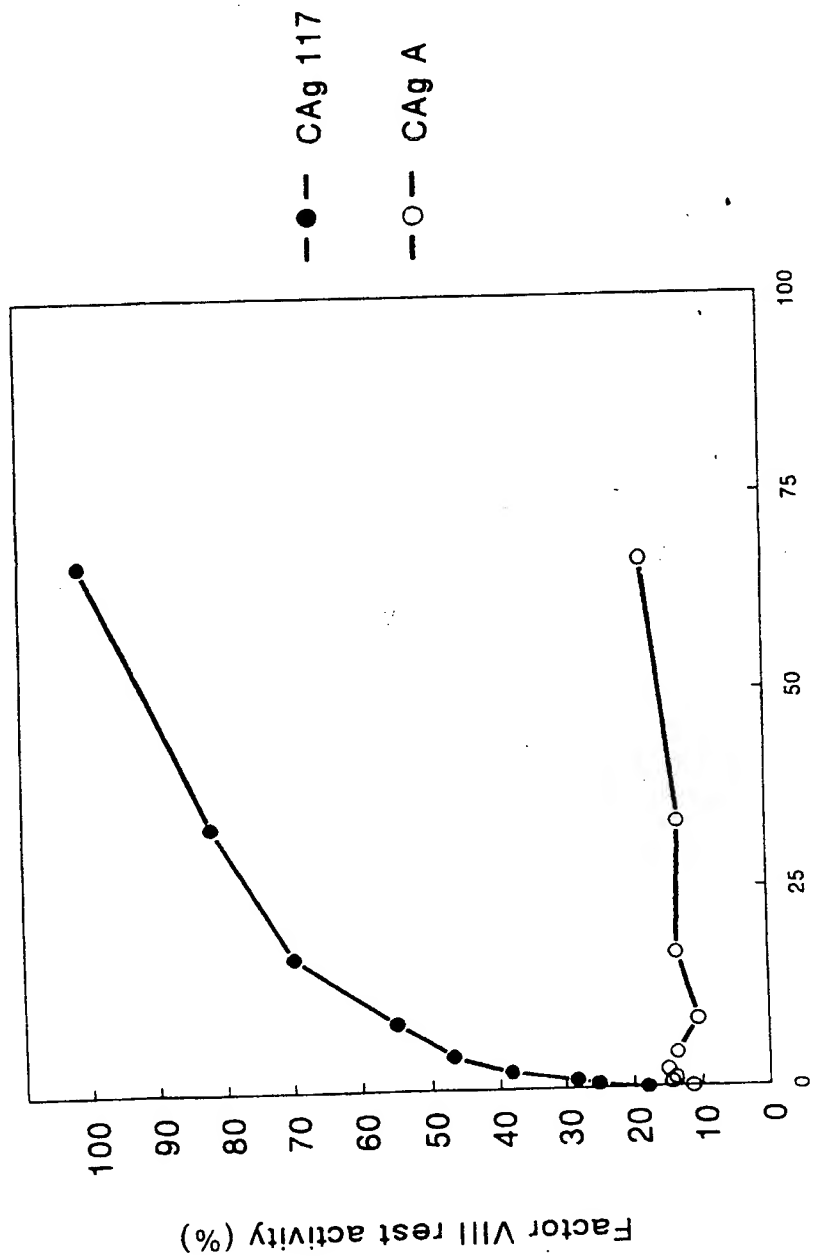
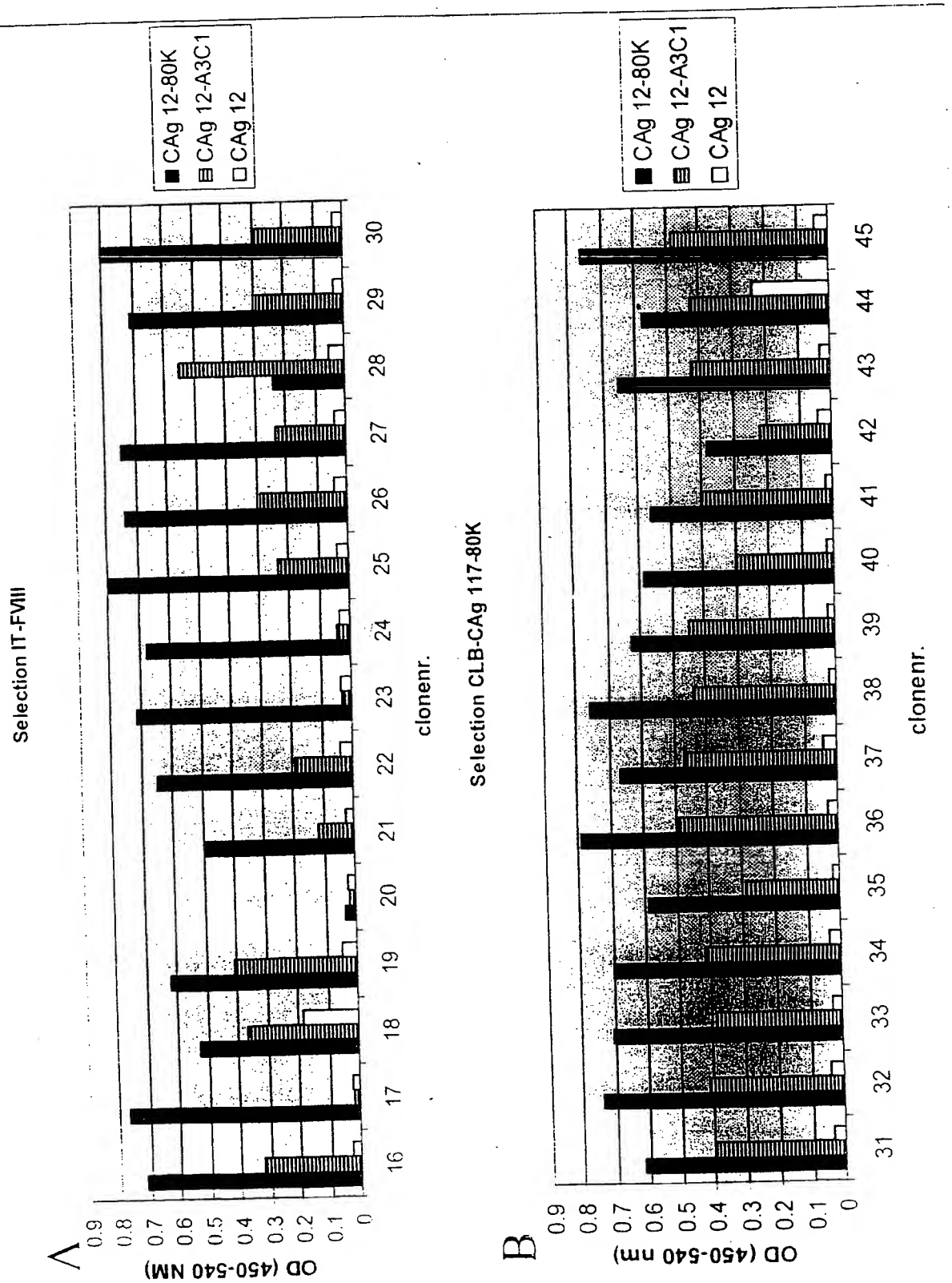


Figure 7B NEUTRALIZATION BY scFv IT-2

Figure 8


A
Selection IT-FVIII
CAg 12-80K
CAg 12-A3C1
CAg 12
OD (450-540 NM)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
clonenr.
B
Selection CLB-CAg 117-80K
CAg 12-80K
CAg 12-A3C1
CAg 12
OD (450-540 nm)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
clonenr.

Deduced protein sequences of isolated FVIII A3-C1 specific scFv

Heavy chains

```
                FR1                  CDR1   FR2          CDR2                    FR3                                  CDR3          FR4
                                                                                                                  1       1     1
                                                                                                                  0       0     1
          1         2         3          4         5         6         7         8         9         0         1         1         2
12345678901234567890123456789012345 67890123456789 012a3456789012345 678901234567890123abc4567890123456 7890abcdefghi12 34567890123
DP-15     QVQLVQSGAEVKKPGASVKVSCKASGYTFT SYDIN WVRQATGQGLEWMG WMNPNSGNTGYAQKFQG RVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
B38       ----L-YA-D-----------T----I-- ----- ------------ --------A-F----K- -L-L--D--T-------RN-E---------- CDTTLLIWFGPAPYNDS WGQGTLV

DP-31     EVQLVESGGGLVQPGRSLRLSCAASGFTFD DYAMH WVRQAPGKGLEWVS GISWNSGSIGYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTALYYCAK D
B18       Q----Q---------K------------G ---I- -------E------ -VT-SGTT--F------ --------------Y--------------L PYINSSNYRRGVAAFDI WGQGTMVTVSS

DP-49     QVQLVESGGGVVQPGRSLRLSCAASGFTFS SYGMH WVRQAPGKGLEWVA VISYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
B35       E---------L----------VD--L--- ----- -------A------ ------ND--------- --A-----A----------TI---------- DLIESNI       AEAL WGQGTLVTVSS

DP-77     EVQLVESGGGLVKPGGSLRLSCAASGFTFS SYSMN WVRQAPGKGLEWVS SISSSSSYIYYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
B04       -----K--E-------------------R R-DIH ----T--------- ----GGN--D------- ---------N-VV----------M---F--- DGTIFGSAATWR AFDI WGRGTMVTVSSG
```

Figure 9A

SUBSTITUTE SHEET (RULE 26)

```
+1  Gln Val Gln Leu Leu Gln Ser Ala Ala Asp  Val Lys Lys Pro Gly Ala Ser
    CAGGTGCAGC TGTTGCAGTC TGCAGCTGAC GTGAAGAAGC CTGGGGCCTC 50
    GTCCACGTCG ACAACGTCAG ACGTCGACTG CACTTCTTCG GACCCCGGAG

+1  Val Lys Val  Ser Cys Thr Ala Ser Gly Tyr Ile Phe Thr  Ser Tyr Asp Ile
    AGTGAAGGTC TCCTGTACGG CTTCTGGATA CATCTTCACC AGTTATGATA 100
    TCACTTCCAG AGGACATGCC GAAGACCTAT GTAGAAGTGG TCAATACTAT

+1  Asn Trp Val Arg Gln Ala  Thr Gly Gln Gly Leu Glu Trp Met Gly Trp
    TCAACTGGGT GCGACAGGCC ACTGGACAAG GGCTTGAGTG GATGGGATGG 150
    AGTTGACCCA CGCTGTCCGG TGACCTGTTC CCGAACTCAC CTACCCTACC

+1  Met Asn Pro Asn Ser Gly Asn Ala Gly Phe  Ala Gln Lys Phe Lys Gly Arg
    ATGAATCCTA ACAGTGGTAA CGCAGGCTTT GCACAGAAGT TTAAGGGCAG 200
    TACTTAGGAT TGTCACCATT GCGTCCGAAA CGTGTCTTCA AATTCCCGTC

+1  Leu Thr Leu  Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr  Met Glu Leu Arg
    ACTCACCTTG ACCAGGGACA CTTCCACAAG CACAGCCTAC ATGGAGCTGA 250
    TGAGTGGAAC TGGTCCCTGT GAAGGTGTTC GTGTCGGATG TACCTCGACT

+1  Arg Leu Glu Ser Glu Asp  Thr Ala Val Tyr Tyr Cys Ala Arg Cys Asp
    GGAGACTGGA ATCTGAGGAC ACGGCCGTGT ATTACTGTGC GAGATGTGAC 300
    CCTCTGACCT TAGACTCCTG TGCCGGCACA TAATGACACG CTCTACACTG

+1  Thr Thr Leu Leu Ile Trp Phe Gly Pro Ala  Pro Tyr Tyr Asp Ser Trp Gly
    ACCACACTCT TAATCTGGTT CGGGCCCGCC CCCTACTATG ACTCCTGGGG 350
    TGGTGTGAGA ATTAGACCAA GCCCGGGCGG GGGATGATAC TGAGGACCCC

+1  Gln Gly Thr  Leu Val
    CCAGGGAACT CTAGTC                                      400
    GGTCCCTTGA GATCAG
```

Figure 9B

```
+1   Gln Val Gln Leu Val Gln Ser Gly Gly Gly  Leu Val Gln Pro Gly Lys Ser
     CAGGTGCAAC TGGTGCAGTC TGGGGGAGGC TTGGTACAGC CTGGCAAGTC 50
     GTCCACGTTG ACCACGTCAG ACCCCCTCCG AACCATGTCG GACCGTTCAG

     Leu Arg Leu  Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly  Asp Tyr Ala Ile
     CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACATTTGGC GATTATGCCA 100
     GGACTCTGAG AGGACACGTC GGAGACCTAA GTGTAAACCG CTAATACGGT

+1   His Trp Val Arg Gln Ala  Pro Gly Glu Gly Leu Glu Trp Val Ser Gly
     TACACTGGGT CCGGCAAGCT CCAGGGGAGG GCCTGGAGTG GGTCTCAGGT 150
     ATGTGACCCA GGCCGTTCGA GGTCCCCTCC CGGACCTCAC CCAGAGTCCA

     Val Thr Trp Ser Gly Thr Thr Ile Gly Phe  Ala Asp Ser Val Lys Gly Arg
     GTTACTTGGA GTGGTACTAC TATAGGCTTT GCGGACTCTG TGAAGGGCCG 200
     CAATGAACCT CACCATGATG ATATCCGAAA CGCCTGAGAC ACTTCCCGGC

     Phe Thr Ile  Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  Leu Tyr Met Asn
     ATTCACCATC TCCAGAGACA ACGCCAAGAA TTCCCTGTAT CTGTACATGA 250
     TAAGTGGTAG AGGTCTCTGT TGCGGTTCTT AAGGGACATA GACATGTACT

+1   Ser Leu Arg Ala Glu Asp  Thr Ala Leu Tyr Tyr Cys Ala Leu Pro Tyr
     ACAGTCTGAG AGCTGAAGAC ACGGCCTTGT ATTATTGTGC CTTACCATAT 300
     TGTCAGACTC TCGACTTCTG TGCCGGAACA TAATAACACG GAATGGTATA

     Ile Asn Ser Ser Asn Tyr Arg Arg Gly Val  Ala Ala Phe Asp Ile Trp Gly
     ATCAACTCGT CCAACTACAG AAGAGGGGTC GCTGCCTTCG ATATCTGGGG 350
     TAGTTGAGCA GGTTGATGTC TTCTCCCCAG CGACGGAAGC TATAGACCCC

+1   Gln Gly Thr  Met Val Thr Val Ser Ser
     CCAAGGGACA ATGGTCACCG TGTCGAGT                          400
     GGTTCCCTGT TACCAGTGGC ACAGCTCA
```

Figure 9C

```
+1   Glu  Val  Gln  Leu  Val  Glu  Ser  Gly  Gly  Gly  Leu  Val  Gln  Pro  Gly  Arg  Ser
     GAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGAGGTC 50
     CTCCACGTCG ACCACCTCAG ACCCCCTCCG AACCATGTCG GACCCTCCAG

+1   _  Leu  Arg  Leu  Ser  Cys  Val  Asp  Ser  Gly  Leu  Thr  Phe  Ser  Ser  Tyr  Gly  Met
     CCTGAGACTC TCCTGTGTAG ACTCTGGACT CACCTTCAGT AGTTATGGCA 100
     GGACTCTGAG AGGACACATC TGAGACCTGA GTGGAAGTCA TCAATACCGT

+1   _  His  Trp  Val  Arg  Gln  Ala  Pro  Gly  Ala  Gly  Leu  Glu  Trp  Val  Ala  Val
     TGCACTGGGT CCGCCAGGCT CCAGGCGCGG GGCTGGAGTG GGTGGCCGTT 150
     ACGTGACCCA GGCGGTCCGA GGTCCGCGCC CCGACCTCAC CCACCGGCAA

-1   Ile  Ser  Tyr  Asp  Gly  Asn  Asp  Lys  Tyr  Tyr  Ala  Asp  Ser  Val  Lys  Gly  Arg
     ATTTCATACG ACGGAAATGA TAAATATTAT GCAGACTCCG TGAAGGGCCG 200
     TAAAGTATGC TGCCTTTACT ATTTATAATA CGTCTGAGGC ACTTCCCGGC

+1   _  Phe  Ala  Ile  Ser  Arg  Asp  Asn  Ala  Lys  Asn  Thr  Leu  Tyr  Leu  Gln  Met  Asn
     ATTCGCCATC TCCAGAGACA ATGCCAAGAA CACGCTGTAT CTGCAAATGA 250
     TAAGCGGTAG AGGTCTCTGT TACGGTTCTT GTGCGACATA GACGTTTACT

+1   _  Ser  Leu  Thr  Ile  Glu  Asp  Thr  Ala  Val  Tyr  Tyr  Cys  Ala  Lys  Asp  Leu
     ACAGCCTGAC AATAGAGGAC ACGGCTGTCT ATTATTGTGC GAAAGATCTC 300
     TGTCGGACTG TTATCTCCTG TGCCGACAGA TAATAACACG CTTTCTAGAG

+1   Ile  Glu  Ser  Asn  Ile  Ala  Glu  Ala  Leu  Trp  Gly  Gln  Gly  Thr  Leu  Val  Thr
     ATAGAATCAA ATATTGCGGA GGCCCTCTGG GGCCAGGGAA CCCTGGTCAC 350
     TATCTTAGTT TATAACGCCT CCGGGAGACC CCGGTCCCTT GGGACCAGTG

+1   _  Val  Ser  Ser                                                    400
     CGTGTCGAGT
     GCACAGCTCA
```

Figure 9D

```
+1  Glu Val Gln Leu Val Lys Ser Gly Glu Gly  Leu Val Lys Pro Gly Gly Ser
    GAGGTGCAGC TGGTGAAGTC TGGGGAAGGC CTGGTCAAGC CTGGGGGGTC 50
    CTCCACGTCG ACCACTTCAG ACCCCTTCCG GACCAGTTCG GACCCCCCAG

-1   Leu Arg Leu  Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg  Arg Tyr Asp Ile
    CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTCAGG AGATATGATA 100
    GGACTCTGAG AGGACACGTC GGAGACCTAA GTGGAAGTCC TCTATACTAT

+1   His Trp Val  Arg Gln Thr  Pro Gly Lys Gly  Leu Glu  Trp Val Ser Ser
    TCCACTGGGT CCGCCAGACT CCAGGGAAGG GCCTGGAGTG GGTCTCATCC 150
    AGGTGACCCA GGCGGTCTGA GGTCCCTTCC CGGACCTCAC CCAGAGTAGG

+1  Ile Ser Ser  Gly Gly Asn  Tyr Ile Asp Tyr  Ala Asp Ser  Val Lys Gly  Arg
    ATCAGTAGTG GTGGTAATTA CATAGACTAC GCAGACTCTG TGAAGGGCCG 200
    TAGTCATCAC CACCATTAAT GTATCTGATG CGTCTGAGAC ACTTCCCGGC

+1   Phe Thr Ile  Ser Arg Asp  Asn Ala Asn  Asn Val Val Tyr  Leu Gln Met Asn
    ATTCACCATC TCCAGAGACA ACGCCAACAA TGTTGTCTAT CTACAAATGA 250
    TAAGTGGTAG AGGTCTCTGT TGCGGTTGTT ACAACAGATA GATGTTTACT

+1   Ser Leu  Arg  Ala Glu Asp  Met Ala Val  Tyr  Phe Cys  Ala Arg Asp Gly
    ACAGCCTGAG AGCCGAGGAC ATGGCTGTCT ATTTCTGTGC GAGAGATGGG 300
    TGTCGGACTC TCGGCTCCTG TACCGACAGA TAAAGACACG CTCTCTACCC

-1  Thr  Ile  Phe  Gly  Ser  Ala  Ala  Thr  Trp  Arg  Ala Phe  Asp  Ile  Trp  Gly  Arg
    ACGATTTTTG GATCGGCGGC GACCTGGCGG GCTTTTGATA TCTGGGGCCG 350
    TGCTAAAAAC CTAGCCGCCG CTGGACCGCC CGAAAACTAT AGACCCCGGC

+1   Gly  Thr  Met  Val  Thr  Val  Ser  Ser
    GGGGACAATG GTCACCGTGT CGAGT                              400
    CCCCTGTTAC CAGTGGCACA GCTCA
```

Figure 9E

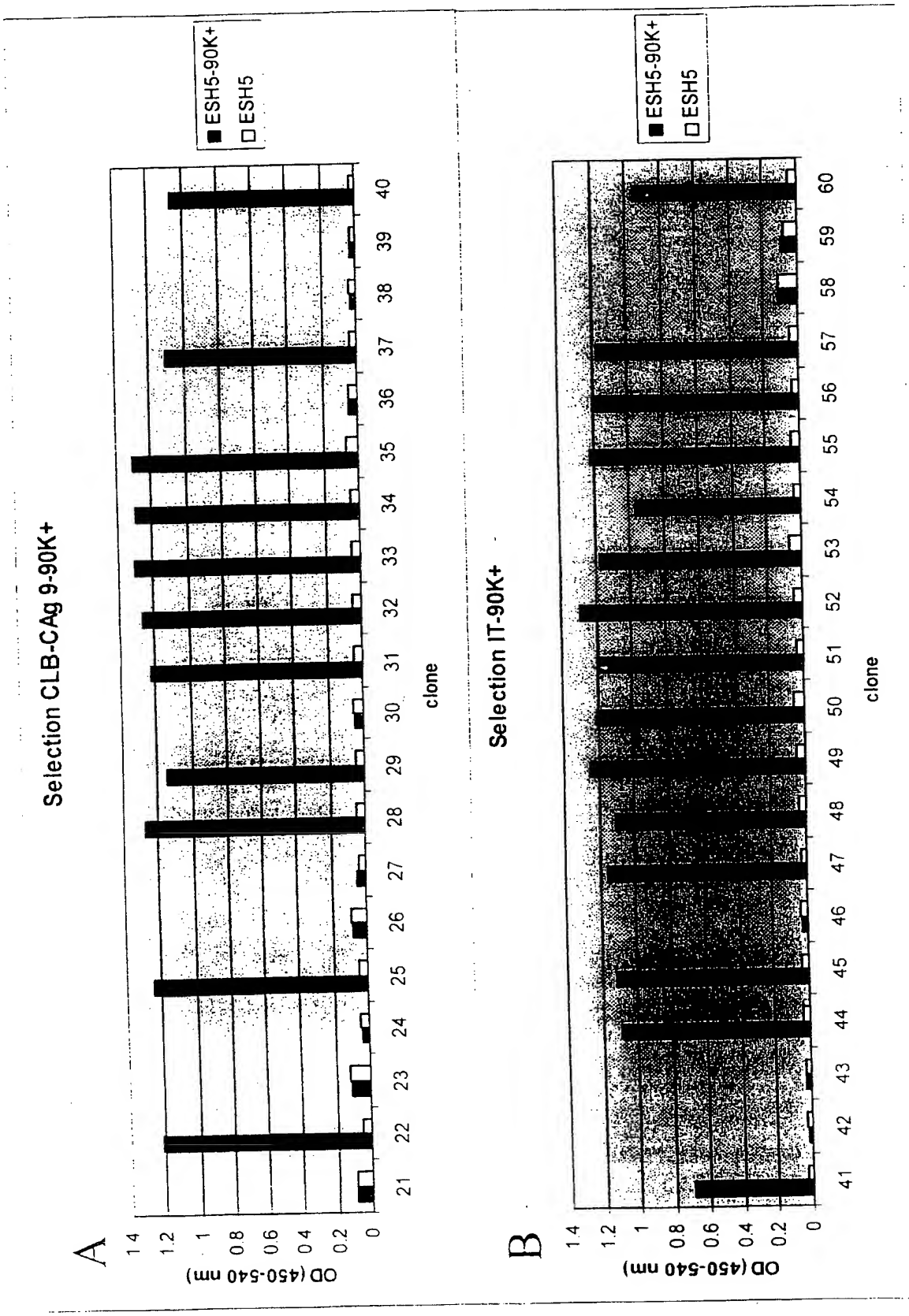

A
Selection CLB-CAg 9-90K+
ESH5-90K+
ESH5
OD (450-540 nm)
clone
B
Selection IT-90K+
ESH5-90K+
ESH5
OD (450-540 nm)
clone

Figure 10

Deduced protein sequences of isolated FVIII A2 specific scFv

Heavy chains

```
                FR1                  CDR1   FR2          CDR2                                FR3                    CDR3        FR4
                                                                                                                  1     1     1
                                                                                                                  0     0     1
          1         2         3          4         5         6         7         8         9          567890abcde12 34567890123
          123456789012345678901234567890 12345 67890123456789 012a3456789012345 678901234567890abc345678901234
DP-10     QVQLVQSGAEVKKPGSSVKVSCKASGGTFS SYAIS WVRQAPGQGLEWMG GIIPIFGTANYAQKFQG RVTITADESTSTAYMELSSLRSEDTAVYYCAR
          ------------------------------ -H--- ------------- D----L--G-------- ------------------T-T---------EL DWFYI         WGQGTMVTVSS

DP-47     EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMS WVRQAPGKGLEWVS AISGSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
          ----V----D-------------------- NF--- -------------A --G-RS-T-F------- ------------V--E----------I----- RGRGGYKYYGMDV WGQGTTVTVSS
```

Figure 11A

SUBSTITUTE SHEET (RULE 26)

```
+1  Gln Val Gln Leu Val Gln Ser Gly Ala Glu  Val Lys Lys Pro Gly Ser Ser
    CAGGTGCAGC TGGTGCAGTC TGGGGCTGAG GTGAAGAAGC CTGGGTCCTC 50
    GTCCACGTCG ACCACGTCAG ACCCCGACTC CACTTCTTCG GACCCAGGAG

+1    Val Lys Val  Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser  Ser His Ala Ile
    GGTGAAGGTC TCCTGCAAGG CTTCTGGAGG CACCTTCAGC AGTCATGCTA 100
    CCACTTCCAG AGGACGTTCC GAAGACCTCC GTGGAAGTCG TCAGTACGAT

+1   Ser Trp Val Arg Gln Ala  Pro Gly Gln Gly Leu Glu Trp Met Gly Asp
    TCAGCTGGGT GCGACAGGCC CCTGGACAAG GGCTTGAGTG GATGGGAGAC 150
    AGTCGACCCA CGCTGTCCGG GGACCTGTTC CCGAACTCAC CTACCCTCTG

+1  Ile Ile Pro Ile Leu Gly Thr Gly Asn Tyr  Ala Gln Lys Phe Gln Gly Arg
    ATCATCCCTA TCCTTGGTAC AGGAAACTAC GCACAGAAGT TCCAGGGCAG 200
    TAGTAGGGAT AGGAACCATG TCCTTTGATG CGTGTCTTCA AGGTCCCGTC

+1   Val Thr Ile  Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr  Met Glu Leu Ser
    AGTCACGATT ACCGCGGACG AGTCCACGAG CACAGCCTAC ATGGAGCTGA 250
    TCAGTGCTAA TGGCGCCTGC TCAGGTGCTC GTGTCGGATG TACCTCGACT

+1   Thr Leu Thr Ser Glu Asp  Thr Ala Val Tyr Tyr Cys Glu Leu Asp Trp
    GCACCCTGAC ATCTGAGGAC ACGGCCGTGT ATTACTGTGA ACTTGACTGG 300
    CGTGGGACTG TAGACTCCTG TGCCGGCACA TAATGACACT TGAACTGACC

-1  Phe Tyr Ile Trp Gly Gln Gly Thr Met Val  Thr Val Ser Ser
    TTCTATATCT GGGGCCAAGG GACAATGGTC ACCGTGTCGA GT          350
    AAGATATAGA CCCCGGTTCC CTGTTACCAG TGGCACAGCT CA
```

Figure 11B

```
+1  Glu Val Gln Leu Val Glu Ser Gly Gly Asp  Leu Val Gln Pro Gly Gly Ser
    GAGGTGCAGC TGGTGGAGTC TGGGGGAGAC TTGGTACAGC CTGGGGGGTC 50
    CTCCACGTCG ACCACCTCAG ACCCCCTCTG AACCATGTCG GACCCCCCAG

+1  Leu Arg Leu  Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  Asn Phe Ala Met
    CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTTAGC AACTTTGCCA 100
    GGACTCTGAG AGGACACGTC GGAGACCTAA GTGGAAATCG TTGAAACGGT

+1  Ser Trp Val Arg Gln Ala  Pro Gly Lys Gly Leu Glu Trp Val Ala Ala
    TGAGCTGGGT CCGCCAGGCT CCCGGGAAGG GGCTGGAGTG GGTCGCGGCT 150
    ACTCGACCCA GGCGGTCCGA GGGCCCTTCC CCGACCTCAC CCAGCGCCGA

+1  Ile Gly Gly Arg Ser Gly Thr Thr Phe Tyr  Ala Asp Ser Val Lys Gly Arg
    ATTGGCGGTA GAAGTGGTAC CACATTCTAC GCGGACTCCG TGAAGGGCCG 200
    TAACCGCCAT CTTCACCATG GTGTAAGATG CGCCTGAGGC ACTTCCCGGC

+1  Phe Thr Ile  Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr  Leu Glu Met Asn
    GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGGTCTAT CTGGAAATGA 250
    CAAGTGGTAG AGGTCTCTGT TAAGGTTCTT GTGCCAGATA GACCTTTACT

+1  Ser Leu Arg Ala Glu Asp  Thr Ala Ile Tyr Tyr Cys Ala Lys Arg Gly
    ACAGTCTGAG AGCCGAGGAC ACAGCCATTT ATTACTGTGC GAAAAGAGGG 300
    TGTCAGACTC TCGGCTCCTG TGTCGGTAAA TAATGACACG CTTTTCTCCC

+1  Arg Gly Gly Tyr Lys Tyr Tyr Gly Met Asp  Val Trp Gly Gln Gly Thr Thr
    CGCGGGGGGT ATAAGTATTA TGGGATGGAC GTCTGGGGCC AGGGGACCAC 350
    GCGCCCCCCA TATTCATAAT ACCCTACCTG CAGACCCCGG TCCCCTGGTG

+1  Val Thr Val  Ser Ser
    GGTCACCGTG TCGAGT                                      400
    CCAGTGGCAC AGCTCA
```

Figure 11C